GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: January 14, 2003, 11:42:22 ; Search time 5.29613 Seconds
(without alignments)
11055.609 Million cell updates/sec

Title: US-09-910-428-1
Perfect score: 26
Sequence: 1 gtgctctaatcttttctggtaccagg 26

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_101002:*
1: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
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22: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
	1	26	100.0	26	24	ABL57124	Cattle growth horm
	2	26	100.0	522	24	ABL57128	Cattle growth horm
	3	26	100.0	540	24	ABL57127	Cattle growth horm
	4	26	100.0	2869	24	ABL57126	Cattle growth horm
c	5	18.2	70.0	1236	22	AAS00247	Bcl-X1-DTR apoptos
c	6	18.2	70.0	1608	18	AAV05129	DNA encoding dipth
c	7	18.2	70.0	1704	22	AAS00248	Bad-DTTR apoptosis
c	8	18.2	70.0	1921	15	AAQ54340	Diphtheria toxin (
c	9	18.2	70.0	1933	15	AAQ54338	Diphtheria toxin d
c	10	18.2	70.0	1936	15	AAQ54337	Diphtheria toxin d
c	11	18.2	70.0	1936	15	AAQ54339	Diphtheria toxin (
c	12	18.2	70.0	1936	15	AAQ54341	Diphtheria toxin (
c	13	18.2	70.0	1936	15	AAQ54342	Diphtheria toxin (
c	14	18.2	70.0	1936	15	AAQ54343	Diphtheria toxin (
c	15	18.2	70.0	1936	15	AAQ54344	Diphtheria toxin (
c	16	18.2	70.0	1936	15	AAQ54345	Diphtheria toxin (
c	17	18.2	70.0	1936	15	AAQ54346	Diphtheria toxin (
c	18	18.2	70.0	1936	15	AAQ54347	Diphtheria toxin (
c	19	18.2	70.0	1936	15	AAQ54348	Diphtheria toxin (
c	20	18.2	70.0	1936	15	AAQ54349	Diphtheria toxin (
c	21	18.2	70.0	1936	15	AAQ54350	Diphtheria toxin (
c	22	18.2	70.0	1940	18	AAT93980	Diphtheria toxin D
c	23	18.2	70.0	1941	11	AAQ05848	Gly(158) Diphtheri
c	24	18.2	70.0	1942	14	AAQ50884	Diphtheria toxin g
c	25	18.2	70.0	1942	15	AAQ54336	Wild type diphther
c	26	18.2	70.0	1942	17	AAY07275	Diphtheria toxin c
c	27	18.2	70.0	1942	21	AAA53821	Wild type diphther
c	28	18.2	70.0	2220	7	AAN60424	Tox228 diptheria t
c	29	18.2	70.0	2220	8	AAN70945	DNA sequence of mo
c	30	18.2	70.0	2221	11	AAQ05917	Sequence contg. to
	31	17.8	68.5	1186	22	AAK75012	Human immature/plasma
	32	17.8	68.5	15399	22	ABA18197	Human nervous syst
	33	17.8	68.5	15399	22	ABA18198	Human nervous syst
	34	17.6	67.7	1779	20	AAV84609	Human secreted pro
	35	17.6	67.7	1779	22	ABA83392	Human secreted pro
	36	17.6	67.7	3059	21	AAF16215	Human prostate can
c	37	17.4	66.9	1617	21	AAC39574	Arabidopsis thalia
	38	17.2	66.2	551	22	ABA61596	Human foetal liver
	39	17.2	66.2	551	22	ABA29272	Probe #7738 for ge
	40	17.2	66.2	551	22	AAK09899	Human brain expres
	41	17.2	66.2	551	22	AAK35792	Human bone marrow
	42	17.2	66.2	551	22	AAI17147	Probe #7070 for ge
	43	17.2	66.2	551	22	AAI41569	Probe #10195 used
	44	17.2	66.2	551	24	ABS10325	Human genome deriv
c	45	17.2	66.2	680	21	AAF13588	Aspergillus oryzae

ALIGNMENTS

RESULT 1
ABL57124
ID ABL57124 standard; DNA; 26 BP.
XX
AC ABL57124;
XX
DT 05-AUG-2002 (first entry)
XX
DE Cattle growth hormone receptor gene T3-repeat 5' PCR primer.
XX
KW Cattle, beef, breeding, growth hormone, somatotropin, receptor;
KW microsatellite, marker-assisted selection; PCR; primer; ss.
XX
OS Bos taurus.
XX
PN CA2312269-A1.
XX
PD 20-JAN-2002.
XX
PF 20-JUL-2000; 2000CA-2312269.
XX
PR 20-JUL-2000; 2000CA-2312269.
XX
PA (UMOR) UNIV MISSOURI.
XX
PI Lucy MC, Lubahn DB, Keisler DH, Shibuya H, Johnson GS, Herring WO;
PI Hale CS;
XX
DR WPI; 2002-417707/45.
XX
PT Obtaining head of beef cattle with genetic predisposition for altered
PT carcass weight, by assaying genetic material from head for polymorphism

```
PT   linked to promoter P1 of exon 1A of bovine growth hormone receptor gene
PT   -
XX
PS   Claim 7; Page 26; 51pp; English.
XX
CC   The present sequence is a primer that corresponds to nucleotides
CC   located 5' to a polymorphic TG repeat microsatellite located 90 bp
CC   upstream from a major transcription start site in the bovine growth
CC   hormone receptor gene (see ABL57124). The TG-repeat microsatellite
CC   can be used as a genetic marker that correlates with cattle growth.
CC   Cattle having at least 12, and preferably 16-20, copies of the TG
CC   dinucleotide repeat marker show increased carcass or weaning weight
CC   compared with cattle having fewer than 12 copies of the TG
CC   dinucleotide repeat. Use of this marker and other genetic markers
CC   in linkage disequilibrium with the locus allows implementation of
CC   selection and breeding schemes for improvement of cattle performance.
CC   Marker assisted selection with the genetic markers avoids the costly
CC   phenotypic testing associated with traditional breeding schemes
XX
SQ   Sequence 26 BP; 4 A; 6 C; 6 G; 10 T; 0 other;

  Query Match             100.0%;  Score 26;  DB 24;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 0.023;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GTGCTCTAATCTTTTCTGGTACCAGC 26
           ||||||||||||||||||||||||||
Db       1 GTGCTCTAATCTTTTCTGGTACCAGC 26


RESULT 2
ABL57128
ID   ABL57128 standard; DNA; 522 BP.
XX
AC   ABL57128;
XX
DT   05-AUG-2002  (first entry)
XX
DE   Cattle growth hormone receptor gene promoter and exon 1A region
XX
KW   Cattle; beef; breeding; growth hormone; somatotropin; receptor;
KW   microsatellite, marker assisted selection, ds.
XX
OS   Bos indicus
XX
FH   Key             Location/Qualifiers
FT   primer_bind     complement (207..232)
FT                   /*tag= a
FT   satellite       234..255
FT                   /*tag= b
FT                   /note= "TG dinucleotide repeat microsatellite"
FT   primer_bind     275..300
FT                   /*tag= c
FT   exon            344..522
FT                   /*tag= d
FT                   /number= 1A
FT   variation       replace(12,C)
FT                   /*tag= e
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(94,C)
FT                   /*tag= f
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(473,G)
FT                   /*tag= g
FT                   /standard_name= "Single nucleotide polymorphism"
XX
PN   CA2312269 A1.
XX
PD   20 JAN 2002.
XX
PF   20 JUL 2000; 2000CA-2312269.
XX
PR   20 JUL 2000; 2000CA-2312269.
XX
PA   (UMOR ) UNIV MISSOURI.
XX
PI   Lucy MC, Lubahn DB, Keisler DH, Shibuya H, Johnson GS, Herring WO;
PI   Hale CS;
XX
DR   WPI; 2002-417707/45.
XX
PT   Obtaining head of beef cattle with genetic predisposition for altered
PT   carcass weight, by assaying genetic material from head for polymorphism
PT   linked to promoter P1 of exon 1A of bovine growth hormone receptor gene
PT   -
XX
PS   Example 2; Fig 3; 51pp; English.
XX
CC   The present sequence is the promoter and exon 1A region of the
CC   bovine growth hormone receptor gene. A polymorphic TG-repeat
CC   microsatellite located 90 bp upstream from a major transcription
CC   start site in the gene is associated with average weaning weight
CC   and carcass weight of cattle. Cattle having at least 12, and
CC   preferably 16-20, copies of the TG dinucleotide repeat marker
CC   show increased carcass or weaning weight compared with cattle
CC   having fewer than 12 copies of the TG dinucleotide repeat. Use of
CC   this marker and other genetic markers in linkage disequilibrium
CC   with the locus allows implementation of selection and breeding
CC   schemes for improvement of cattle performance. Other genetic
CC   markers may include polymorphisms such as the C/A polymorphic
CC   site in exon 1A. The A allele (found in indicine cattle) contains
CC   a DraI restriction site that is not present in the C allele (found
CC   in taurine cattle). This difference can be used in a PCR/RFLP
CC   assay to distinguish the respective alleles. The 2 i/c upstream
CC   polymorphic sites could similarly be used. Marker assisted
CC   selection with the genetic markers avoids the costly phenotypic
CC   testing associated with traditional breeding schemes.
XX
SQ   Sequence 522 BP; 124 A; 121 C; 136 G; 141 T; 0 other;

  Query Match             100.0%;  Score 26;  DB 24;  Length 522;
  Best Local Similarity   100.0%;  Pred. No. 0.084;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GTGCTCTAATCTTTTCTGGTACCAGG 26
           ||||||||||||||||||||||||||
Db     207 GTGCTCTAATCTTTTCTGGTACCAGG 232


RESULT 3
ABL57127
ID   ABL57127 standard; DNA; 540 BP.
XX
AC   ABL57127;
XX
DT   05-AUG-2002  (first entry)
XX
DE   Cattle growth hormone receptor gene promoter and exon 1A region.
XX
KW   Cattle; beef; breeding; growth hormone; somatotropin; receptor;
KW   microsatellite, marker assisted selection, ds.
XX
OS   Bos taurus.
XX
FH   Key             Location/Qualifiers
FT   primer_bind     complement (207..232)
FT                   /*tag= a
FT   satellite       234..273
FT                   /*tag= b
FT                   /note= "TG dinucleotide repeat microsatellite"
FT   primer_bind     293..318
FT                   /*tag= c
FT   exon            362..540
FT                   /*tag= d
FT                   /number= 1A
FT   variation       replace(12,T)
```

```
FT                   /*tag= e
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(94,T)
FT                   /*tag= f
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(491,A)
FT                   /*tag= g
FT                   /standard_name= "Single nucleotide polymorphism"
XX
PN   CA2312269 A1.
XX
PD   20-JAN-2002.
XX
PF   20-JUL-2000; 2000CA-2312269.
XX
PR   20-JUL-2000; 2000CA-2312269.
XX
PA   (UMOR ) UNIV MISSOURI.
XX
PI   Lucy MC, Lubahn DB, Keisler DH, Shibuya H, Johnson GS, Herring WO;
PI   Hale CS;
XX
DR   WPI, 2002-417707/45.
XX
PT   Obtaining head of beef cattle with genetic predisposition for altered
PT   carcass weight, by assaying genetic material from head for polymorphism
PT   linked to promoter P1 of exon 1A of bovine growth hormone receptor gene
PT   -
XX
PS   Example 2; Fig 3; 51pp; English.
XX
CC   The present sequence is the promoter and exon 1A region of the
CC   bovine growth hormone receptor gene. A polymorphic TG repeat
CC   microsatellite located 90 bp upstream from a major transcription
CC   start site in the gene is associated with average weaning weight
CC   and carcass weight of cattle. Cattle having at least 12, and
CC   preferably 16-20, copies of the TG dinucleotide repeat marker
CC   show increased carcass or weaning weight compared with cattle
CC   having fewer than 12 copies of the TG dinucleotide repeat. Use of
CC   this marker and other genetic markers in linkage disequilibrium
CC   with the locus allows implementation of selection and breeding
CC   schemes for improvement of cattle performance. Other genetic
CC   markers may include polymorphisms such as the G/A polymorphic
CC   site in exon 1A. The A allele (found in indicine cattle) contains
CC   a DraI restriction site that is not present in the G allele (found
CC   in taurine cattle). This difference can be used in a PCR/RFLP
CC   assay to distinguish the respective alleles. The 2 T/C upstream
CC   polymorphic sites could similarly be used. Marker-assisted
CC   selection with the genetic markers avoids the costly phenotypic
CC   testing associated with traditional breeding schemes.
XX
SQ   Sequence 540 BP; 123 A; 123 C; 146 G; 148 T; 0 other;

  Query Match           100.0%;  Score 26;  DB 24;  Length 540;
  Best Local Similarity  100.0%;  Pred. No. 0.034;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GTGCTCTAATCTTTTCTGGTACCAGG 26
           ||||||||||||||||||||||||||
Db     207 GTGCTCTAATCTTTTCTGGTACCAGG 232


RESULT 4
ABL57126
ID   ABL57126 standard; DNA; 2869 BP.
XX
AC   ABL57126;
XX
DT   05-AUG-2002  (first entry)
XX
DE   Cattle growth hormone receptor gene promoter and exon 1A region.
XX
KW   Cattle; beef; breeding; growth hormone; somatotropin; receptor;
KW   microsatellite; marker-assisted selection; ds.
XX
OS   Bos taurus.
XX
FH   Key             Location/Qualifiers
FT   primer_bind     complement (2580..2605)
FT                   /*tag= a
FT   satellite       2607..2646
FT                   /*tag= b
FT                   /note= "TG dinucleotide repeat microsatellite"
FT   primer_bind     2666..2680
FT                   /*tag= c
FT   exon            2735..2869
FT                   /*tag= d
FT                   /number= 1A
XX
PN   CA2312269-A1.
XX
PD   20-JAN-2002.
XX
PF   20-JUL-2000; 2000CA-2312269.
XX
PR   20-JUL-2000; 2000CA-2312269.
XX
PA   (UMOR ) UNIV MISSOURI.
XX
PI   Lucy MC, Lubahn DB, Keisler DH, Shibuya H, Johnson GS, Herring WO;
PI   Hale CS;
XX
DR   WPI; 2002-417707/45.
XX
PT   Obtaining head of beef cattle with genetic predisposition for altered
PT   carcass weight, by assaying genetic material from head for polymorphism
PT   linked to promoter P1 of exon 1A of bovine growth hormone receptor gene
PT   -
XX
PS   Claim 3; Page 41-43; 51pp; English.
XX
CC   The present sequence is the promoter and exon 1A region of the
CC   bovine growth hormone receptor gene. A polymorphic TG-repeat
CC   microsatellite located 90 bp upstream from a major transcription
CC   start site in the gene is associated with average weaning weight
CC   and carcass weight of cattle. Cattle having at least 12, and
CC   preferably 16-20, copies of the TG dinucleotide repeat marker
CC   show increased carcass or weaning weight compared with cattle
CC   having fewer than 12 copies of the TG dinucleotide repeat. Use of
CC   this marker and other genetic markers in linkage disequilibrium
CC   with the locus allows implementation of selection and breeding
CC   schemes for improvement of cattle performance. Marker-assisted
CC   selection with the genetic markers avoids the costly phenotypic
CC   testing associated with traditional breeding schemes.
XX
SQ   Sequence 2869 BP; 657 A; 640 C; 582 G; 990 T; 0 other;

  Query Match           100.0%;  Score 26;  DB 24;  Length 2869;
  Best Local Similarity  100.0%;  Pred. No. 0.043;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GTGCTCTAATCTTTTCTGGTACCAGG 26
           ||||||||||||||||||||||||||
Db    2580 GTGCTCTAATCTTTTCTGGTACCAGG 2605


RESULT 5
AAS00247/c
ID   AAS00247 standard; DNA; 1236 BP.
XX
AC   AAS00247;
XX
DT   31-MAY-2001  (first entry)
XX
DE   Bcl-Xl-DTR apoptosis-modifying fusion protein, DNA sequence.
XX
```

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KW   Human; Bcl X1 DTR, apoptosis, cancer, spinal muscular atrophy, ds.
KW   diphtheria toxin receptor binding domain; DTR; neoplasm; tumour;
KW   hyper proliferation; Alzheimer's disease; neurodegenerative disorder;
KW   transient ischaemic neuronal injury, stroke, spinal cord injury,
KW   Huntington's disease.
XX
OS   Chimeric   Homo sapiens.
OS   Chimeric   Corynebacterium diptheriae.
OS   Chimeric   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..1236
FT                   /*tag= a
FT                   /product= "Bcl-Xl-DTR fusion protein"
FT                   /note= "DTR is diphtheria toxin receptor binding domain"
FT   misc_feature    7..36
FT                   /*tag= b
FT                   /note= "10x Histidine tag"
FT   misc_feature    61..759
FT                   /*tag= c
FT                   /note= "Bcl-Xl gene from codon 1-233"
FT   misc_feature    760..777
FT                   /*tag= d
FT                   /note= "Linker DNA, linking Bcl-Xl to DTR"
FT   misc_feature    778..1236
FT                   /*tag= e
FT                   /note= "DTR, diphtheria toxin receptor binding domain"
XX
PN   WO200112661-A2.
XX
PD   22 FEB 2001.
XX
PF   15 AUG 2000; 2000WO-US22294.
XX
PR   16 AUG 1999;   99US-0149220.
XX
PA   (HARD ) HARVARD COLLEGE.
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Youle RJ, Liu X, Collier RJ;
XX
DR   WPI; 2001-218343/22.
DR   P-PSDB; AAU00219.
XX
PT   Novel fusion protein for modifying apoptosis in target cell and
PT   reducing apoptosis after transient ischaemic neuronal injury, has two
PT   domains which targets protein to a cell and modifies apoptotic response
PT   of cell
XX
PS   Claim 5; Page 54-56; 65pp; English.
XX
CC   The sequence represents the coding sequence of Bcl-Xl-DTR apoptosis-
CC   modifying fusion protein comprising human Bcl-Xl sequence fused via a
CC   short linker to diphtheria toxin receptor binding domain (DTR). The
CC   functional apoptosis-modifying fusion protein is capable of binding a
CC   target cell and integrating into or crossing a cellular membrane of the
CC   target cell. The apoptosis modifying fusion protein comprises at least
CC   two domains: the DTR domain, which targets the fusion protein to the
CC   target cell and the Bcl-XL domain, which modifies an apoptotic response
CC   of the target cell. The fusion protein is useful for modifying
CC   (inhibiting or enhancing) apoptosis in a target cell, such as neuron,
CC   lymphocyte, cancer, neoplasm, macrophage, epithelial, stem, tumour or
CC   hyper-proliferative cell or an adipocyte. It is also useful for reducing
CC   apoptosis in a subject after transient ischaemic neuronal injury,
CC   especially spinal cord injury. The fusion protein may be used to treat
CC   various diseases and injury conditions through inhibition or enhancement
CC   of apoptotic cellular response, including neurodegenerative disorders
CC   such as Alzheimer's disease, Huntington's disease, spinal muscular
CC   atrophy, stroke episodes and unregulated cell growth as in tumours and
CC   various cancers. The apoptosis modifying fusion protein can be delivered
CC   effectively throughout the body and targeted to selective tissue and
CC   cells.
XX
SQ   Sequence 1236 BP; 317 A; 291 C; 343 G; 285 T; 0 other;

  Query Match             70.0%;  Score 18.2;  DB 22;  Length 1236;
  Best Local Similarity   87.0%;  Pred. No. 1.3e+02;
  Matches   20;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 GTGCTCTAATCTTTTCTGGTACC 23
           ||| |||| | ||||||||||||
Db    1188 GTCATCTACTGTTTTCTGGTACC 1166


RESULT 6
AAV05129/c
ID   AAV05129 standard; cDNA; 1608 BP.
XX
AC   AAV05129;
XX
DT   18-MAY-1998  (first entry)
XX
DE   DNA encoding diptheria toxin.
XX
KW   Cholesteryl ester transfer protein, CETP; cholesteryl ester;
KW   high density lipoprotein; HDL; very low density lipoprotein; VLDL;
KW   low density lipoprotein; LDL; T cell epitope; antibody;
KW   DNA plasmid-based vaccine; broad range helper T cell epitope;
KW   treatment; cardiovascular disease; ss.
XX
XX
OS   Corynebacterium diphtheriae.
XX
PN   WO9741227-A1.
XX
PD   06-NOV-1997.
XX
PF   01-MAY-1997;   97WO-US07294.
XX
PR   21-FEB-1997;   97US-0802967.
PR   01-MAY-1996;   96US-0640713.
XX
PA   (TCEL-) T CELL SCI INC.
XX
PI   Thomas LJ;
XX
DR   WPI; 1997-549731/50.
DR   P-PSDB; AAW46448.
XX
PT   DNA plasmid based vaccine encodes CETP B cell and helper T cell
PT   epitope(s) - used for elevating high density lipoprotein levels, and
PT   for treating cardiovascular disease
XX
PS   Disclosure; Pages 40-42; 67pp; English.
XX
CC   The present sequence encodes a diphtheria toxin. Regions of the
CC   present sequence can be utilised as broad range helper T cell epitopes
CC   in DNA plasmid based vaccines against cholesteryl ester transfer
CC   proteins (CETPs). CETPs mediate the transfer of cholesteryl esters from
CC   high density lipoprotein (HDL) to very low density lipoprotein (VLDL) and
CC   low density lipoprotein (LDL), and vice versa. An increased CETP activity
CC   produces an atherogenic lipoprotein profile and induces atherosclerosis.
CC   A DNA plasmid-based vaccine comprises sequences encoding at least one
CC   B cell epitope of CETP linked in frame with at least one segment encoding
CC   a broad range helper T cell epitope. The vaccines can be used to elevate
CC   the ratio of circulating HDL to circulating LDL, VLDL or total
CC   cholesterol in a human. It can also be used for decreasing the level of
CC   endogenous CETP activity in a human. The vaccine can be used to produce
CC   anti-CETP antibodies in vivo and for treating cardiovascular disease.
XX
SQ   Sequence 1608 BP; 492 A; 294 C; 382 G; 440 T; 0 other;

  Query Match             70.0%;  Score 18.2;  DB 18;  Length 1608;
  Best Local Similarity   87.0%;  Pred. No. 1.3e+02;
  Matches   20;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;
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Qy       1 GTCCTCTAATCTTTTCTGCTACC 23
           ||| |||| | ||||||||||||
Db    1560 GTGATCTACTGTTTTCTGGTACC 1538


RESULT 7
AAS00248/c
ID   AAS00248 standard; DNA; 1704 BP.
XX
AC   AAS00248;
XX
DT   31-MAY-2001  (first entry)
XX
DE   Bad-DTTR apoptosis-modifying fusion protein, DNA sequence.
XX
KW   Mouse; Bad-DTTR; apoptosis; cancer; spinal muscular atrophy; ds;
KW   diphtheria toxin receptor binding domain; DTTR; neoplasm; tumour;
KW   hyper-proliferation, Alzheimer's disease; neurodegenerative disorder;
KW   transient ischaemic neuronal injury; stroke; spinal cord injury;
KW   Huntington's disease, diphtheria toxin translocation domain.
XX
OS   Chimeric - Mus sp.
OS   Chimeric - Corynebacterium diptheriae.
OS   Chimeric - Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..1704
FT                   /*tag= a
FT                   /product= "Bad-DTTR fusion protein"
FT                   /note= "DTTR is diphtheria toxin translocation domain"
FT   misc_feature    7..36
FT                   /*tag= b
FT                   /note= "10x histidine tag"
XX
PN   WO200112661-A2.
XX
PD   22-FEB-2001.
XX
PF   15-AUG-2000; 2000WO-US22293.
XX
PR   16-AUG-1999;   99US-0149220.
XX
PA   (HARD ) HARVARD COLLEGE.
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Youle RJ, Liu X, Collier RJ;
XX
DR   WPI; 2001-218343/22.
DR   P-PSDB; AAU00220.
XX
PT   Novel fusion protein for modifying apoptosis in target cell and
PT   reducing apoptosis after transient ischaemic neuronal injury, has two
PT   domains which targets protein to a cell and modifies apoptotic response
PT   of cell -
XX
PS   Claim 5; Page 57-59; 65pp; English.
XX
CC   The sequence represents the coding sequence of Bad-DTTR apoptosis-
CC   modifying fusion protein comprising Bad gene sequence fused via a short
CC   linker to diphtheria toxin translocation domain (DTTR). The
CC   functional apoptosis-modifying fusion protein is capable of binding a
CC   target cell and integrating into or crossing a cellular membrane of the
CC   target cell. The apoptosis-modifying fusion protein comprises at least
CC   two domains: the DTR domain, which targets the fusion protein to the
CC   target cell and the Bcl-XL domain, which modifies an apoptotic response
CC   of the target cell. The fusion protein is useful for modifying
CC   (inhibiting or enhancing) apoptosis in a target cell, such as neuron,
CC   lymphocyte, cancer, neoplasm, macrophage, epithelial, stem, tumour or
CC   hyper-proliferative cell or an adipocyte. It is also useful for reducing
CC   apoptosis in a subject after transient ischaemic neuronal injury,
CC   especially spinal cord injury. The fusion protein may be used to treat
CC   various diseases and injury conditions through inhibition or enhancement
CC   of apoptotic cellular response, including neurodegenerative disorders
CC   such as Alzheimer's disease, Huntington's disease, spinal muscular
CC   atrophy, stroke episodes and unregulated cell growth as in tumours and
CC   various cancers. The apoptosis modifying fusion protein can be delivered
CC   effectively throughout the body and targeted to selective tissue and
CC   cells.
XX
SQ   Sequence 1704 BP; 470 A; 395 C; 444 G; 395 T; 0 other;

  Query Match             70.0%;  Score 18.2;  DB 22;  Length 1704;
  Best Local Similarity   87.0%;  Pred. No. 1.3e+02;
  Matches   20;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 GTGCTCTAATCTTTTCTGGTACC 23
           ||| |||| | ||||||||||||
Db    1656 GTGATCTACTGTTTTCTGGTACC 1634


RESULT 8
AAQ54340/c
ID   AAQ54340 standard; DNA; 1921 BP.
XX
AC   AAQ54340;
XX
DT   22-JUN-1994  (first entry)
XX
DE   Diphtheria toxin (delta-142 to 148) mutant coding sequence.
XX
KW   DT; protein exotoxin; NAD-dependent ADP-ribosyltransferase; vaccine;
KW   diphtheria toxoid; deletion mutant; mutein; variant; double mutant;
KW   reversion mutation; site-directed mutagenesis; ds.
XX
OS   Corynebacterium diphtheriae.
XX
FH   Key             Location/Qualifiers
FT   CDS             312..1898
FT                   /*tag= a
FT                   /product= delta-142_to_-148_diphtheria_toxin
FT                   /note= "single chain translation product is readily
FT                           cleaved to form two subunits (A and B), linked
FT                           by a disulphide bond; wild-type codons 142
FT                           to 148 have been deleted"
XX
PN   WO9325210-A.
XX
PD   23-DEC-1993.
XX
PF   17-MAY-1993;   93WO-US04606.
XX
PR   18-JUN-1992;   92US-0901712.
XX
PA   (HARD ) HARVARD COLLEGE.
XX
PI   Collier RJ, Killeen K, Mekalanos J;
XX
DR   WPI; 1994-007178/01.
DR   P-PSDB; AAR44892.
XX
PT   New DNA encoding diphtheria toxin deletion mutants - with no
PT   toxicity and low risk of reversion, and derived toxoids and
PT   transformed cells, useful in vaccines
XX
PS   Claim 4; ; 42pp; English.
XX
CC   Oligonucleotide directed mutagenesis of the wild-type diphtheria
CC   gene (specifically the region encoding the DT A fragment) results
CC   in deletion of the codons for Val 147 and active site residue
CC   Glu-148 and opt. deletion or substitution of other active residues.
CC   The resulting muteins are not toxic, making them useful in diphtheria
CC   vaccines. The risk of reversion to toxicity is much lower for the
CC   147-148 double mutants than for the prior art 148 single mutant,
CC   while their immunogenicity is not impaired. The specification
CC   includes the wild-type DT coding sequence but does not include any
CC   mutant sequences; the wild-type sequence was modified according to
```

```
CC   the description in the claims to give AAQ54340.
XX
SQ   Sequence 1921 BP; 571 A; 357 C; 464 G; 530 T; 0 other;

  Query Match             70.0%;  Score 18.2;  DB 15;  Length 1921;
  Best Local Similarity   87.0%;  Pred. No. 1.3e+02;
  Matches   20;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 GTGCTCTAATCTTTTCTGGTACC 23
           ||| |||| | ||||||||||||
Db    1850 GTGATCTACTGTTTTCTGGTACC 1828


RESULT 9
AAQ54338/c
ID   AAQ54338 standard; DNA; 1933 BP.
XX
AC   AAQ54338;
XX
DT   22-JUN-1994  (first entry)
XX
DE   Diphtheria toxin delta-142-147-148 mutant coding sequence.
XX
KW   DT; protein exotoxin; NAD-dependent ADP-ribosyltransferase; vaccine;
KW   diphtheria toxoid; deletion mutant; mutein; variant; double mutant;
KW   reversion mutation; site-directed mutagenesis; ds.
XX
OS   Corynebacterium diphtheriae.
XX
FH   Key             Location/Qualifiers
FT   CDS             312..1910
FT                   /*tag= a
FT                   /product= "delta-142-147-148_diphtheria_toxin
FT                   /note= "single chain translation product is readily
FT                          cleaved to form two subunits (A and B), linked
FT                          by a disulphide bond; wild-type codons 142
FT                          (Glu), 147(Val) and 148(Glu) have been deleted"
XX
PN   WO9325210-A.
XX
PD   23-DEC-1993.
XX
PF   17-MAY-1993;   93WO-US04606.
XX
PR   18-JUN-1992;   92US-0901712.
XX
PA   (HARO ) HARVARD COLLEGE.
XX
PI   Collier RJ,  Killeen K,  Mekalanos J;
XX
DR   WPI; 1994-007178/01
DR   P-PSDB; AAR44890.
XX
PT   New DNA encoding diphtheria toxin deletion mutants - with no
PT   toxicity and low risk of reversion, and derived toxoids and
PT   transformed cells, useful in vaccines
XX
PS   Claim 3; ; 42pp; English.
XX
CC   Oligonucleotide directed mutagenesis of the wild-type diphtheria
CC   gene (specifically the region encoding the DT-A fragment) results
CC   in deletion of the codons for Val-147 and active site residue
CC   Glu 148 and opt. deletion or substitution of other active residues.
CC   The resulting muteins are not toxic, making them useful in diphtheria
CC   vaccines. The risk of reversion to toxicity is much lower for the
CC   147-148 double mutants than for the prior art 148 single mutant,
CC   while their immunogenicity is not impaired. The specification
CC   includes the wild type DT coding sequence but does not include any
CC   mutant sequences; the wild type sequence was modified according to
CC   the description in the claims to give AAQ54338.
XX
SQ   Sequence 1933 BP; 573 A; 359 C; 468 G; 533 T; 0 other;

  Query Match             70.0%;  Score 18.2;  DB 15;  Length 1933;
  Best Local Similarity   87.0%;  Pred. No. 1.3e+02;
  Matches   20;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 GTGCTCTAATCTTTTCTGGTACC 23
           ||| |||| | ||||||||||||
Db    1862 GTGATCTACTGTTTTCTGGTACC 1840


RESULT 10
AAQ54337/c
ID   AAQ54337 standard; DNA; 1936 BP.
XX
AC   AAQ54337;
XX
DT   22-JUN-1994  (first entry)
XX
DE   Diphtheria toxin delta-147-148 mutant coding sequence.
XX
KW   DT; protein exotoxin; NAD-dependent ADP-ribosyltransferase; vaccine;
KW   diphtheria toxoid; deletion mutant; mutein; variant; double mutant;
KW   reversion mutation; site-directed mutagenesis; ds.
XX
OS   Corynebacterium diphtheriae.
XX
FH   Key             Location/Qualifiers
FT   CDS             312..1914
FT                   /*tag= a
FT                   /product= delta-147-148_diphtheria_toxin
FT                   /note= "single chain translation product is readily
FT                          cleaved to form two subunits (A and B), linked
FT                          by a disulphide bond; wild-type codons 147
FT                          (Val) and 148(Glu) have been deleted"
XX
PN   WO9325210-A.
XX
PD   23-DEC-1993.
XX
PF   17-MAY-1993;   93WO-US04606.
XX
PR   18-JUN-1992;   92US-0901712.
XX
PA   (HARO ) HARVARD COLLEGE.
XX
PI   Collier RJ,  Killeen K,  Mekalanos J;
XX
DR   WPI; 1994-007178/01.
DR   P-PSDB; AAR44889.
XX
PT   New DNA encoding diphtheria toxin deletion mutants - with no
PT   toxicity and low risk of reversion, and derived toxoids and
PT   transformed cells, useful in vaccines
XX
PS   Claim 1; ; 42pp; English.
XX
CC   Oligonucleotide-directed mutagenesis of the wild-type diphtheria
CC   gene (specifically the region encoding the DT-A fragment) results
CC   in deletion of the codons for Val-147 and active site residue
CC   Glu-148 and opt. deletion or substitution of other active residues.
CC   The resulting muteins are not toxic, making them useful in diphtheria
CC   vaccines. The risk of reversion to toxicity is much lower for the
CC   147-148 double mutants than for the prior art 148 single mutant,
CC   while their immunogenicity is not impaired. The specification
CC   includes the wild type DT coding sequence but does not include any
CC   mutant sequences; the wild type sequence was modified according to
CC   the description in the claims to give AAQ54337.
XX
SQ   Sequence 1936 BP; 574 A; 359 C; 470 G; 533 T; 0 other;

  Query Match             70.0%;  Score 18.2;  DB 15;  Length 1936;
  Best Local Similarity   87.0%;  Pred. No. 1.3e+02;
  Matches   20;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;
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Qy       1 GTGCTCTAATCTTTTCTGGTACC 23
           ||| |||| | ||||||||||||
Db    1865 GTGATCTACTGTTTTCTGGTACC 1843


RESULT 11
AAQ54339/c
ID   AAQ54339 standard; DNA; 1936 BP.
XX
AC   AAQ54339;
XX
DT   22-JUN-1994  (first entry)
XX
DE   Diphtheria toxin (delta-147-148; E142X) mutant coding sequence.
XX
KW   DT; protein exotoxin; NAD-dependent ADP ribosyltransferase; vaccine;
KW   diphtheria toxoid; deletion mutant; mutein; variant; double mutant;
KW   reversion mutation; site-directed mutagenesis; ds.
XX
OS   Corynebacterium diphtheriae.
XX
FH   Key             Location/Qualifiers
FT   misc_difference 735..737
FT                   /*tag= a
FT                   /note= "wild-type GAG (Glu) codon substd  by codon
FT                   for any other amino acid"
FT   CDS             311..1913
FT                   /*tag= b
FT                   /product= delta 147 148,E142X_diphtheria_toxin
FT                   /note= "single chain translation product is readily
FT                   cleaved to form two subunits (A and B), linked
FT                   by a disulphide bond; wild type codons 147
FT                   (Val) and 148(Glu) have been deleted and
FT                   142(Glu) has been altered"
XX
PN   WO9325210-A.
XX
PD   23-DEC-1993.
XX
PF   17-MAY-1993;   93WO-US04606.
XX
PR   18-JUN-1992;   92US-0901712.
XX
PA   (HARD ) HARVARD COLLEGE.
XX
PI   Collier RJ,  Killeen K,  Mekalanos J;
XX
DR   WPI; 1994-007178/01.
DR   P-PSDB; AAR44891.
XX
PT   New DNA encoding diphtheria toxin deletion mutants - with no
PT   toxicity and low risk of reversion, and derived toxoids and
PT   transformed cells, useful in vaccines
XX
PS   Claim 3; ; 42pp; English.
XX
CC   Oligonucleotide-directed mutagenesis of the wild-type diphtheria
CC   gene (specifically the region encoding the DT-A fragment); results
CC   in deletion of the codons for Val 147 and active site residue
CC   Glu-148 and opt. deletion or substitution of other active residues.
CC   The resulting muteins are not toxic, making them useful in diphtheria
CC   vaccines. The risk of reversion to toxicity is much lower for the
CC   147-148 double mutants than for the prior art 148 single mutant,
CC   while their immunogenicity is not impaired. The specification
CC   includes the wild-type DT coding sequence but does not include any
CC   mutant sequences; the wild-type sequence was modified according to
CC   the description in the claims to give AAQ54339.
XX
SQ   Sequence 1936 BP; 573 A; 359 C; 468 G; 533 T; 3 other;

  Query Match             70.0%;  Score 18.2;  DB 15;  Length 1936;
  Best Local Similarity   87.0%;  Pred. No. 1.3e+02;
  Matches   20;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 GTGCTCTAATCTTTTCTGGTACC 23
           ||| |||| | ||||||||||||
Db    1865 GTGATCTACTGTTTTCTGGTACC 1843


RESULT 12
AAQ54341/c
ID   AAQ54341 standard; DNA; 1936 BP.
XX
AC   AAQ54341;
XX
DT   22-JUN-1994  (first entry)
XX
DE   Diphtheria toxin (delta-147-148; H21X) mutant coding sequence.
XX
KW   DT; protein exotoxin; NAD-dependent ADP-ribosyltransferase; vaccine;
KW   diphtheria toxoid; deletion mutant; mutein; variant; double mutant;
KW   reversion mutation; site-directed mutagenesis; ds.
XX
OS   Corynebacterium diphtheriae.
XX
FH   Key             Location/Qualifiers
FT   misc_difference 372..374
FT                   /*tag= a
FT                   /note= "wild-type CAC (His) codon is replaced by
FT                   codon for any other amino acid or is absent"
FT   CDS             312..1913
FT                   /*tag= b
FT                   /product= diphtheria_toxin_mutant
FT                   /note= "single chain translation product is readily
FT                   cleaved to form two subunits (A and B), linked
FT                   by a disulphide bond; wild-type codons 147
FT                   (Val) and 148(Glu) have been deleted and
FT                   the His(21) codon is altered or deleted"
XX
PN   WO9325210-A.
XX
PD   23-DEC-1993.
XX
PF   17-MAY-1993;   93WO-US04606.
XX
PR   18-JUN-1992;   92US-0901712.
XX
PA   (HARD ) HARVARD COLLEGE.
XX
PI   Collier RJ,  Killeen K,  Mekalanos J;
XX
DR   WPI; 1994-007178/01.
DR   P-PSDB; AAR44893.
XX
PT   New DNA encoding diphtheria toxin deletion mutants - with no
PT   toxicity and low risk of reversion, and derived toxoids and
PT   transformed cells, useful in vaccines
XX
PS   Claim 7; ; 42pp; English.
XX
CC   Oligonucleotide-directed mutagenesis of the wild-type diphtheria
CC   gene results in deletion of the codons for Val-147 and active site
CC   residue Glu-148; opt. a third residue which is essential for the full
CC   toxic activity of wild type DT is deleted or altered to encode a
CC   different amino acid residue. The third residue can be in the
CC   fragment A (see AAQ54341-7) or in the fragment B (see AAQ54348-Q54350)
CC   portion of DT. The resulting muteins are not toxic, making them useful
CC   in diphtheria vaccines. The risk of reversion to toxicity is much
CC   lower for the 147-148 double mutants than for the prior art 148 single
CC   mutant, while their immunogenicity is not impaired. The specification
CC   includes the wild-type DT coding sequence but does not include any
CC   mutant sequences; the wild-type sequence was modified according to
CC   the description in the claims to give AAQ54341.
XX
SQ   Sequence 1936 BP; 573 A; 357 C; 470 G; 533 T; 3 other;
```

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  Query Match             70.0%;  Score 18.2;  DB 15;  Length 1936;
  Best Local Similarity   87.0%;  Pred. No. 1.3e+02;
  Matches   20;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 GTGCTCTAATCTTTTCTGGTACC 23
           ||| |||| | ||||||||||||
Db    1865 GTGATCTACTGTTTTCTGGTACC 1843


RESULT 13
AAQ54342/c
ID   AAQ54342 standard; DNA; 1936 BP.
XX
AC   AAQ54342;
XX
DT   22-JUN-1994  (first entry)
XX
DE   Diphtheria toxin (delta 147-148; G22X) mutant coding sequence.
XX
KW   DT; protein exotoxin; NAD dependent ADP ribosyltransferase; vaccine;
KW   diphtheria toxoid; deletion mutant; mutein; variant; double mutant;
KW   reversion mutation; site directed mutagenesis; ds.
XX
OS   Corynebacterium diphtheriae.
XX
FH   Key             Location/Qualifiers
FT   misc_difference 475..477
FT                   /*tag= a
FT                   /note= "wild type GGT (Gly) codon is replaced by
FT                         codon for any other amino acid or is absent
FT                         N.B. the amino acid at position 22 of the
FT                         wild-type DT is given as Glu in the claims"
FT   CDS             312..1913
FT                   /*tag= b
FT                   /product= diphtheria_toxin_mutant
FT                   /note= "single chain translation product is readily
FT                         cleaved to form two subunits (A and B), linked
FT                         by a disulphide bond, wild type codons 147
FT                         (Val) and 148(Glu) have been deleted and
FT                         the Gly(22) codon is altered or deleted"
XX
PN   WO9325210 A.
XX
PD   23 DEC 1993.
XX
PF   17 MAY 1993;   93WO US04606.
XX
PR   18 JUN 1992;   92US 0901712.
XX
PA   (HARD ) HARVARD COLLEGE.
XX
PI   Collier RJ,  Killeen K,  Mekalanos J;
XX
DR   WPI; 1994 007178/01.
DR   P PSDB; AAR44894.
XX
PT   New DNA encoding diphtheria toxin deletion mutants - with no
PT   toxicity and low risk of reversion, and derived toxoids and
PT   transformed cells, useful in vaccines
XX
PS   Claim 7; ; 42pp; English.
XX
CC   Oligonucleotide-directed mutagenesis of the wild-type diphtheria
CC   gene results in deletion of the codons for Val-147 and active site
CC   residue Glu 148; opt. a third residue which is essential for the full
CC   toxic activity of wild type DT is deleted or altered to encode a
CC   different amino acid residue. The third residue can be in the
CC   fragment A (see AAQ54341-7) or in the fragment B (see AAQ54348-Q54350)
CC   portion of DT. The resulting muteins are not toxic, making them useful
CC   in diphtheria vaccines. The risk of reversion to toxicity is much
CC   lower for the 147-148 double mutants than for the prior art 148 single
CC   mutant, while their immunogenicity is not impaired. The specification
CC   includes the wild type DT coding sequence but does not include any
CC   mutant sequences, the wild type sequence was modified according to
CC   the description in the claims to give AAQ54342.
XX
SQ   Sequence 1936 BP; 574 A; 359 C; 467 G; 534 T; 4 other;

  Query Match             70.0%;  Score 18.2;  DB 15;  Length 1936;
  Best Local Similarity   87.0%;  Pred. No. 1.3e+02;
  Matches   20;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 GTGCTCTAATCTTTTCTGGTACC 23
           ||| |||| | ||||||||||||
Db    1865 GTGATCTACTGTTTTCTGGTACC 1843


RESULT 14
AAQ54343/c
ID   AAQ54343 standard; DNA; 1936 BP.
XX
AC   AAQ54343;
XX
DT   22-JUN-1994  (first entry)
XX
DE   Diphtheria toxin (delta-147-148; K39X) mutant coding sequence.
XX
KW   DT; protein exotoxin; NAD-dependent ADP-ribosyltransferase; vaccine;
KW   diphtheria toxoid; deletion mutant; mutein; variant; double mutant;
KW   reversion mutation; site directed mutagenesis; ds.
XX
OS   Corynebacterium diphtheriae.
XX
FH   Key             Location/Qualifiers
FT   misc_difference 426..428
FT                   /*tag= a
FT                   /note= "wild type AAA (Lys) codon is replaced by
FT                         codon for any other amino acid or is absent"
FT   CDS             312..1913
FT                   /*tag= b
FT                   /product= diphtheria_toxin_mutant
FT                   /note= "single chain translation product is readily
FT                         cleaved to form two subunits (A and B), linked
FT                         by a disulphide bond; wild type codons 147
FT                         (Val) and 148(Glu) have been deleted and
FT                         the Lys(39) codon is altered or deleted"
XX
PN   WO9325210-A.
XX
PD   23-DEC-1993.
XX
PF   17-MAY-1993;   93WO-US04606.
XX
PR   18-JUN-1992;   92US-0901712.
XX
PA   (HARD ) HARVARD COLLEGE.
XX
PI   Collier RJ,  Killeen K,  Mekalanos J;
XX
DR   WPI; 1994-007178/01.
DR   P PSDB; AAR44895.
XX
PT   New DNA encoding diphtheria toxin deletion mutants - with no
PT   toxicity and low risk of reversion, and derived toxoids and
PT   transformed cells, useful in vaccines
XX
PS   Claim 7; ; 42pp; English.
XX
CC   Oligonucleotide directed mutagenesis of the wild type diphtheria
CC   gene results in deletion of the codons for Val-147 and active site
CC   residue Glu 148; opt. a third residue which is essential for the full
CC   toxic activity of wild type DT is deleted or altered to encode a
CC   different amino acid residue. The third residue can be in the
CC   fragment A (see AAQ54341-7) or in the fragment B (see AAQ54348-Q54350)
CC   portion of DT. The resulting muteins are not toxic, making them useful
CC   in diphtheria vaccines. The risk of reversion to toxicity is much
```

```
CC   lower for the 147-148 double mutants than for the prior art 148 single
CC   mutant, while their immunogenicity is not impaired. The specification
CC   includes the wild type DT coding sequence but does not include any
CC   mutant sequences, the wild type sequence was modified according to
CC   the description in the claims to give AAQ54343.
XX
SQ   Sequence 1936 BP; 571 A; 359 C; 470 G; 533 T; 3 other;

  Query Match             70.0%;  Score 18.2;  DB 15;  Length 1936;
  Best Local Similarity   87.0%;  Pred. No. 1.3e+02;
  Matches   20;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 GTGCTCTAATCTTTTCTGGTACC 23
           ||| |||| | ||||||||||||
Db    1865 GTGATCTACTGTTTTCTGGTACC 1843


RESULT 15
AAQ54344/c
ID   AAQ54344 standard; DNA; 1936 BP.
XX
AC   AAQ54344;
XX
DT   22-JUN-1994  (first entry)
XX
DE   Diphtheria toxin (delta-147-148; G52X) mutant coding sequence.
XX
KW   DT; protein exotoxin; NAD-dependent ADP-ribosyltransferase; vaccine;
KW   diphtheria toxoid; deletion mutant, mutein; variant; double mutant;
KW   reversion mutation; site-directed mutagenesis; ds.
XX
OS   Corynebacterium diphtheriae.
XX
FH   Key             Location/Qualifiers
FT   misc_difference 465..467
FT                   /*tag=  a
FT                   /note= "wild-type GGG (Gly) codon is replaced by
FT                          codon for any other amino acid or is absent"
FT   CDS             312..1913
FT                   /*tag=  b
FT                   /product= diphtheria_toxin_mutant
FT                   /note= "single chain translation product is readily
FT                          cleaved to form two subunits (A and B), linked
FT                          by a disulphide bond; wild-type codons 147
FT                          (Val) and 148(Glu) have been deleted and
FT                          the Gly(52) codon is altered or deleted"
XX
PN   WO9325210-A.
XX
PD   23-DEC-1993.
XX
PF   17-MAY-1993;   93WO-US04606.
XX
PR   18-JUN-1992;   92US-0901712.
XX
PA   (HARD ) HARVARD COLLEGE.
XX
PI   Collier RJ.  Killeen K.  Mekalanos J;
XX
DR   WPI; 1994-007178/01.
DR   P-PSDB; AAR44896.
XX
PT   New DNA encoding diphtheria toxin deletion mutants - with no
PT   toxicity and low risk of reversion, and derived toxoids and
PT   transformed cells, useful in vaccines
XX
PS   Claim 7; ; 42pp; English.
XX
CC   Oligonucleotide-directed mutagenesis of the wild-type diphtheria
CC   gene results in deletion of the codons for Val-147 and active site
CC   residue Glu-148; opt. a third residue which is essential for the full
CC   toxic activity of wild-type DT is deleted or altered to encode a
CC   different amino acid residue. The third residue can be in the
CC   fragment A (see AAQ54341-7) or in the fragment B (see AAQ54348-054350)
CC   portion of DT. The resulting muteins are not toxic, making them useful
CC   in diphtheria vaccines. The risk of reversion to toxicity is much
CC   lower for the 147-148 double mutants than for the prior art 148 single
CC   mutant, while their immunogenicity is not impaired. The specification
CC   includes the wild-type DT coding sequence but does not include any
CC   mutant sequences; the wild-type sequence was modified according to
CC   the description in the claims to give AAQ54344.
XX
SQ   Sequence 1936 BP; 574 A; 359 C; 467 G; 533 T; 3 other;

  Query Match             70.0%;  Score 18.2;  DB 15;  Length 1936;
  Best Local Similarity   87.0%;  Pred. No. 1.3e+02;
  Matches   20;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 GTGCTCTAATCTTTTCTGGTACC 23
           ||| |||| | ||||||||||||
Db    1865 GTGATCTACTGTTTTCTGGTACC 1843


Search completed: January 14, 2003, 11:52:35
Job time : 7.29613 secs
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